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CLMPTO

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01/18/05

Claims 1 – 27 have been cancelled

Claims 28 – 49 have been added

28. An enzyme, designated as phospholipid:diacylglycerol acyltransferase (PDAT), catalyzing in an acyl-CoA-independent reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol and comprising an amino acid sequence as set forth in SEQ ID NO:2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof.

29. An enzyme according to claim 28, comprising an amino acid sequence encoded through a nucleotide sequence as set forth in SEQ ID NO:1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1.

30. An enzyme according to claim 28, comprising an amino acid sequence as set forth in SEQ ID NO. 16, 20 or 22, or a functional fragment, derivate, allele, homolog or isoenzyme thereof.

31. An enzyme according to claim 28, comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 6, 8, 13, 14, 15, 17, 18, 25 and 27, a functional fragment, derivate, allele, homolog or isoenzyme thereof.

32. An enzyme according to claim 28, comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence.

33. A nucleotide sequence according to claim 32, selected

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from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 10, 11, 19, 21, 23, 24, 29 and 30, or a portion, derivate, allele or homolog thereof.

34. A partial nucleotide sequence corresponding to a full length nucleotide sequence according to claim 32, selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 and 31, or a portion, derivate, allele or homolog thereof.

35. A nucleotide sequence according to claim 32, comprising a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31.

36. A gene construct comprising a nucleotide sequence as set forth in SEQ ID No. 1, or a homologous nucleotide sequence which is at least about 40% identical to the nucleotide sequence of SEQ ID No. 1, which is operably linked to a heterologous nucleic.

37. A vector comprising a gene construct according to claim 36, or the nucleotide sequence as set forth in SEQ ID No. 1, or a homologous nucleotide sequence which is at least about 40% identical to the nucleotide sequence of SEQ ID No. 1.

38. A vector according to claim 37, which is an expression vector.

39. A vector according to claim 37, further comprising a selectable marker gene and/or nucleotide sequences for the replication in a host cell or the integration into the genome of the host cell.

40. A transgenic cell or organism comprising one or more of the following:

a) a nucleotide sequence a_1 to a_n ,

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b) a gene construct b_1), and

c) a vector c_1),

wherein

a_1) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,

a_2) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,

a_3) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;

a_4) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,

b_1) is a gene construct comprising a nucleotide sequence a_1), operably linked to a heterologous nucleic acid, and

c_1) is a vector comprising a gene construct b_1), or a nucleotide sequence a_1).

41. A transgenic cell or organism according to claim 40, which is an eucaryotic cell or organism.

42. A transgenic cell or organism according to claim 40, which is a yeast cell or a plant cell or a plant.

43. A transgenic cell or organism according to claim 40 having an altered biosynthetic pathway for the production of

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triacylglycerol, characterized by the prevention of accumulation of undesirable fatty acids, which are harmful if present in high amounts in membrane lipids.

44. A transgenic cell or organism according to claim 40 having an altered, increased oil content.

45. A transgenic cell or organism according to claim 40, wherein the activity of PDAT is altered, characterized by an alteration in gene expression, catalytic activity and/or regulation of activity of the enzyme.

46. A process for the production of triacylglycerol, comprising growing a transgenic cell or organism according to claim 40 under conditions whereby the said nucleotide sequence

- a₁) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,
 - a₂) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,
 - a₃) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;
 - a₄) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,
- is expressed.

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47. Triacylglycerols produced by a process according to claim 46.

48. Use of a nucleotide sequence selected from the group of
- a₁) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,
 - a₂) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,
 - a₃) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;
 - a₄) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,
- or an enzyme selected from the group of
- d₁) is an enzyme, designated as phospholipid:diacylglycerol acyltransferase (PDAT), catalyzing in an acyl-CoA-independent reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol and comprising an amino acid sequence as set forth in SEQ ID NO. 2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof,
 - d₂) is an enzyme d₁), comprising an amino acid sequence as set forth in SEQ ID NO. 16, 20 or 22, or a functional fragment,

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derivate, allele, homolog or isoenzyme thereof,
d₁) is an enzyme d₁), comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 6, 8, 13, 14, 15, 17, 18, 25 and 27, or a functional fragment, derivate, allele, homolog or isoenzyme thereof, for the production of triacylglycerol and/or triacylglycerols with uncommon fatty acids, comprising medium chain fatty acids, hydroxylated fatty acids, epoxygenated fatty acids and acetylenic fatty acids.

49. Use of a nucleotide sequence selected from the group of
- a₁) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,
 - a₂) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,
 - a₃) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;
 - a₄) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,
- or an enzyme selected from the group of
- d₁) is an enzyme, designated as phospholipid:diacylglycerol acyltransferase (PDAT), catalyzing in an acyl-CoA-independent

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reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol and comprising an amino acid sequence as set forth in SEQ ID NO. 2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof,

d₂) is an enzyme d₁), comprising an amino acid sequence as set forth in SEQ ID NO. 16, 20 or 22, or a functional fragment, derivate, allele, homolog or isoenzyme thereof,

d₃) is an enzyme d₁), comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 6, 8, 13, 14, 15, 17, 18, 25 and 27, or a functional fragment, derivate, allele, homolog or isoenzyme thereof,

for the transformation of any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism.